



SEQUENCE LISTING

<110> MAYER, BRUCE
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KIRCHAUSEN, TOMAS

<120> FUSION PROTEIN AND USES THEREOF

<130> 701039-050001-C

<140> 10/027,770

<141> 2001-12-20

<150> PCT/US00/17929

<151> 2000-06-29

<150> 60/141,896

<151> 1999-06-30

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 809

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: DNA encoding 3DX,
a second-generation ScFv derived from monoclonal
antibody 9E10

<220>

<221> CDS

<222> (1)..(807)

<400> 1

gga	tct	acc	atg	gcc	gag	gtg	aag	ctg	gtg	gaa	tct	ggg	gga	gac	tta	48
Gly	Ser	Thr	Met	Ala	Glu	Val	Lys	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	
1				5				10					15			

gtg	aag	cct	gga	ggg	tcc	ctg	aaa	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	96
Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	
			20					25					30			

act	ttc	agt	cac	tat	ggc	atg	tct	tgg	gtt	cgc	cag	act	cca	gac	aag	144
Thr	Phe	Ser	His	Tyr	Gly	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Asp	Lys	
		35					40					45				

agg	ctc	gag	tgg	gtc	gca	acc	att	ggg	agt	cgt	ggg	act	tac	acc	cac	192
Arg	Leu	Glu	Trp	Val	Ala	Thr	Ile	Gly	Ser	Arg	Gly	Thr	Tyr	Thr	His	
		50				55					60					

tat	cca	gac	agt	gtg	aag	gga	cga	ttc	acc	atc	tcc	aga	gac	aat	gac	240
Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Asp	
		65				70				75					80	

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aag aac gcc ctg tac ctg caa atg aac agt ctg cgg act gaa gac aca 288
Lys Asn Ala Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr
      85                      90                      95

gcc atg tat tac tgt gta aga aaa agt gaa ttt tat tac tac ggt aat 336
Ala Met Tyr Tyr Cys Val Arg Lys Ser Glu Phe Tyr Tyr Tyr Gly Asn
      100                      105                      110

acc tac tat tac tct gct atg gac tac tgg ggt caa gga gcc tca gtc 384
Thr Tyr Tyr Tyr Ser Ala Met Asp Tyr Trp Gly Gln Gly Ala Ser Val
      115                      120                      125

acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt gac tct ggc ggt 432
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Asp Ser Gly Gly
      130                      135                      140

ggc ggt tcg gac att gtg ctg acc caa tct cca gct tct ttg gct gta 480
Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
      145                      150                      155                      160

tct cta gga cag agg gcc acc atc tcc tgc aga gcc agc gaa agt gtt 528
Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val
      165                      170                      175

gat aat tat ggc ttt agt ttt atg aac tgg ttc caa cag aaa cca gga 576
Asp Asn Tyr Gly Phe Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly
      180                      185                      190

cag cca ccc aaa ctc ctc atc tat gct aca tcc aac cga gga tcc ggg 624
Gln Pro Pro Lys Leu Leu Ile Tyr Ala Thr Ser Asn Arg Gly Ser Gly
      195                      200                      205

gtc cct gcc agg ttt agt ggc agt ggg tct ggg aca gac ttc agc ctc 672
Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu
      210                      215                      220

aac atc cat cct gta gag gag gat gac tct gca atg tat ttc tgt cag 720
Asn Ile His Pro Val Glu Glu Asp Asp Ser Ala Met Tyr Phe Cys Gln
      225                      230                      235                      240

caa act aag gag gtt ccg tgg acg ttc ggt gga ggc acc aag ctg gaa 768
Gln Thr Lys Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
      245                      250                      255

atc aaa cgg gct gat gct gca cca act gta tcc gcg gcc gc 809
Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ala Ala
      260                      265

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<210> 2

<211> 269

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 3DX, a
second-generation ScFv derived from monoclonal
antibody 9E10

<400> 2

Gly	Ser	Thr	Met	Ala	Glu	Val	Lys	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu
1				5					10					15	
Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe
			20					25						30	
Thr	Phe	Ser	His	Tyr	Gly	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Asp	Lys
			35				40					45			
Arg	Leu	Glu	Trp	Val	Ala	Thr	Ile	Gly	Ser	Arg	Gly	Thr	Tyr	Thr	His
	50					55					60				
Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Asp
65					70					75					80
Lys	Asn	Ala	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Thr	Glu	Asp	Thr
				85					90					95	
Ala	Met	Tyr	Tyr	Cys	Val	Arg	Lys	Ser	Glu	Phe	Tyr	Tyr	Tyr	Gly	Asn
			100					105						110	
Thr	Tyr	Tyr	Tyr	Ser	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Ala	Ser	Val
		115					120					125			
Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Asp	Ser	Gly	Gly
	130					135					140				
Gly	Gly	Ser	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val
145					150					155					160
Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	Ser	Val
				165					170					175	
Asp	Asn	Tyr	Gly	Phe	Ser	Phe	Met	Asn	Trp	Phe	Gln	Gln	Lys	Pro	Gly
			180					185					190		
Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Thr	Ser	Asn	Arg	Gly	Ser	Gly
		195					200					205			
Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ser	Leu
	210					215					220				
Asn	Ile	His	Pro	Val	Glu	Glu	Asp	Asp	Ser	Ala	Met	Tyr	Phe	Cys	Gln
225					230					235					240
Gln	Thr	Lys	Glu	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu
				245					250					255	
Ile	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ala	Ala			
			260					265							

<210> 3

<211> 9

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Epitope to the
12CA5 antibody

<400> 3

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 4

<211> 7

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Short
motif

<400> 4

Pro Glu Arg Pro Pro Lys Pro
1 5

<210> 5

<211> 269

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 3DX, a
second-generation ScFv derived from monoclonal
antibody 9E10 with site directed mutagenesis

<400> 5

Gly Ser Thr Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Asp Leu
1 5 10 15

Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe
20 25 30

Thr Phe Ser His Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys
35 40 45

Arg Leu Glu Trp Val Ala Thr Ile Gly Ser Arg Gly Thr Tyr Thr His
50 55 60

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp
65 70 75 80

Lys Asn Ala Leu Tyr Leu Gln Met Asn Ser Leu Lys Ser Glu Asp Thr
85 90 95

Ala Met Tyr Tyr Cys Ala Arg Arg Ser Glu Phe Tyr Tyr Tyr Gly Asn
100 105 110

Thr Tyr Tyr Tyr Ser Ala Met Asp Tyr Trp Gly Gln Gly Ala Ser Val
115 120 125

Thr	Val	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	
130						135				140					
Gly	Gly	Ser	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val
145					150					155					160
Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	Ser	Val
				165					170					175	
Asp	Asn	Tyr	Gly	Phe	Ser	Phe	Met	Asn	Trp	Phe	Gln	Gln	Lys	Pro	Gly
			180					185					190		
Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ile	Ser	Asn	Arg	Gly	Ser	Gly
		195					200					205			
Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ser	Leu
	210					215					220				
Asn	Ile	His	Pro	Val	Glu	Glu	Asp	Asp	Pro	Ala	Met	Tyr	Phe	Cys	Gln
225					230					235					240
Gln	Thr	Lys	Glu	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu
				245					250					255	
Ile	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ala	Ala			
			260					265							